APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/644,456		Vered Hornik	2254-031	2896

28765   7590   11/04/2002

WINSTON & STRAWN
PATENT DEPARTMENT
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WASHINGTON, DC 20005-3502

EXAMINER
BORIN, MICHAEL L

ART UNIT	PAPER NUMBER
1631	

DATE MAILED: 11/04/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

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OCT 3 1 2002

TECH CENTER 1600/2900

1600

RAW SEQUENCE LISTING   DATE: 10/24/2002
PATENT APPLICATION: US/09/644,456A   TIME: 14:30:37

Input Set : A:\#724253 v1 - sequence listing text.txt
Output Set: N:\CRF4\10242002\I644456A.raw

```
   4 <110> APPLICANT: HORNIK, V. and HADAS, E.
   6 <120> TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE
   7        CYCLIZED INTERLEUKIN-6 ANTAGONISTS
   9 <130> FILE REFERENCE: 87534-3100
  11 <140> CURRENT APPLICATION NUMBER: US 09/644,456A
  12 <141> CURRENT FILING DATE: 2000-08-024
E--> 14 <160> NUMBER OF SEQ ID NOS: (82) 83 (see below)
  16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
 756 <210> SEQ ID NO: 83        last sequence in submitted file
 757 <211> LENGTH: 6
 758 <212> TYPE: PRT
 759 <213> ORGANISM: homo sapiens
 761 <220> FEATURE:
 762 <221> NAME/KEY: misc_feature
 763 <222> LOCATION: (4) .. (4)
 764 <223> OTHER INFORMATION: ornithine
 766 <400> SEQUENCE: 83
W--> 767 Lys Lys Ala Xaa Trp Phe
E--> 768 1     (5)       5      misaligned amino acid numbers
 776 (NY:724253.1)                (see item 3 on Erra Summary Sheet)
                delete
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/644,456A

DATE: 10/24/2002
TIME: 14:30:39

Input Set : A:\#724253 v1 - sequence listing text.txt
Output Set: N:\CRF4\10242002\I644456A.raw

L:12 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0
L:768 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:83
L:14 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (82) Counted (83)

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/644,456A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.